In the Specification:

Please amend the specification as shown:

Please delete the description for Figure 1 on page 8, and replace it with the following description:

Figure 1 is a schematic diagram illustrating a method for generating a peptide internal standard for a protein or modified protein to be detected and/or quantified **(Peptides shown are disclosed as SEQ ID NOS 4 and 5, respectively in order of appearance)**.

Please delete the description for Figures 5A-5C on page 9, and replace it with the following description:

Figure 5A shows a peptide internal standard suitable for use in detecting and/or quantitating a protein comprising the amino acid sequence GFTALK **(SEQ ID NO: 1)**. The upper panel of the Figure shows the native tryptic peptide. The lower portion of the Figure shows a peptide internal standard corresponding to this peptide which comprises a stable isotope (^{13}C). As can be seen from the Figure, the stable isotope provides a characteristic mass difference in the two peptides without altering the essential chemical structure of the peptide. Figure 5B shows a peptide internal standard suitable for use in detecting a phosphorylated form of a protein comprising the amino acid sequence GFTALK **(SEQ ID NO: 1)**. Figure 5C shows a peptide internal standard suitable for use in detecting a methylated form of the amino acid sequence GFTALK **(SEQ ID NO: 1)**.

Please delete the description for Figure 6 on page 9, and replace it with the following description:

Figure 6 shows diagnostic peptide fragmentation signatures obtained for two peptides comprising the sequences ALELFR **(SEQ ID NO: 2)** and LFTGHPETLEK **(SEQ ID NO: 3)**, respectively, from the myoglobin protein. Each peptide produces a characteristic signature ion that can be used to detect and/or quantify myoglobin in a sample of cellular proteins. Providing both peptide internal standards together in an assay can provide an additional control for quantification.